This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Gregory, Richard J.
Wills, Ken N.
Maneval, Daniel C.

(ii) TITLE OF INVENTION: Recombinant Adenoviral Vector and Methods of Use

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Campbell and Flores
(B) STREET: 4370 La Jolla Village Drive, Suite 700
(C) CITY: San Diego
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92122

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/328,673
(B) FILING DATE: 25-OCT-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/233,777
(B) FILING DATE: 19-MAY-1994

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/142,669
(B) FILING DATE: 25-OCT-1993

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Campbell, Cathryn A.
(B) REGISTRATION NUMBER: 31,815
(C) REFERENCE/DOCKET NUMBER: P-CJ 1192

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619) 535-9001
(B) TELEFAX: (619) 535-8949

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGCCACCGAG GGACCTGAGC GAGTC 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCTGGGAAG GGACAGAAGA 20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGCGCTAGCT CTGCCCCAAA GAGCT 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

100
101
102
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
104
105 CGCGGTACCC TCGAGTCTAG ATATTGCCAG TGGTGGAAG 39
106
107 (2) INFORMATION FOR SEQ ID NO:5:
108
109 (i) SEQUENCE CHARACTERISTICS:
110 (A) LENGTH: 35 base pairs
111 (B) TYPE: nucleic acid
112 (C) STRANDEDNESS: single
113 (D) TOPOLOGY: linear
114
115
116
117 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
118
119 CGTGCGGCCG CTGGAGGACT TTGAGGATGT CTGTC 35
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121 (2) INFORMATION FOR SEQ ID NO:6:
122
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 33 base pairs
125 (B) TYPE: nucleic acid
126 (C) STRANDEDNESS: single
127 (D) TOPOLOGY: linear
128
129
130
131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
132
133 CGCTCTAGAG AGACCAGTTA GGAAGTTTTC GCA 33
134
135 (2) INFORMATION FOR SEQ ID NO:7:
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137 (i) SEQUENCE CHARACTERISTICS:
138 (A) LENGTH: 2995 base pairs
139 (B) TYPE: nucleic acid
140 (C) STRANDEDNESS: single
141 (D) TOPOLOGY: linear
142
143
144 (ix) FEATURE:
145 (A) NAME/KEY: CDS
146 (B) LOCATION: 139..2922
147
148
149 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
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151 TTCCGGTTTT TCTCAGGGGA CGTTGAAATT ATTTTTGTAA CGGGAGTCGG GAGAGGACGG 60
152

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153  GGCGTGCCCC GCGTGCGCGC GCGTCGTCCT CCCCGGCGCT CCTCCACAGC TCGCTGGCTC      120
154
155  CCGCCGCGGA AAGGCGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG GCC GCC        171
156                      Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
157                        1               5                  10
158
159  ACC GCC GCC GCT GCC GCC GCG GAA CCC CCG GCA CCG CCG CCG CCG CCC        219
160  Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
161              15                  20                  25
162
163  CCT CCT GAG GAG GAC CCA GAG CAG GAC AGC GGC CCG GAG GAC CTG CCT        267
164  Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
165           30                  35                  40
166
167  CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA        315
168  Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
169       45                  50                  55
170
171  TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGG        363
172  Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
173   60                  65                  70                  75
174
175  TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GGA GTA TTG GGA GGT TAT        411
176  Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
177                    80                  85                  90
178
179  ATT CAA AAG AAA AAG GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA        459
180  Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
181              95                  100                 105
182
183  GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC        507
184  Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
185          110                 115                 120
186
187  ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT        555
188  Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
189      125                 130                 135
190
191  ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT        603
192  Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
193  140                 145                 150                 155
194
195  GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT        651
196  Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
197                  160                 165                 170
198
199  ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT        699
200  Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
201              175                 180                 185
202
203  GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG        747
204  Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
205          190                 195                 200
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206
207   GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG       795
208   Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
209       205                 210                 215
210
211   CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC       843
212   Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
213   220                 225                 230                 235
214
215   AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA       891
216   Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
217                 240                 245                 250
218
219   ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA       939
220   Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
221             255                 260                 265
222
223   GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT       987
224   Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
225         270                 275                 280
226
227   AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT      1035
228   Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
229       285                 290                 295
230
231   ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA      1083
232   Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
233   300                 305                 310                 315
234
235   AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA      1131
236   Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
237                 320                 325                 330
238
239   GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT      1179
240   Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
241             335                 340                 345
242
243   ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT      1227
244   Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
245         350                 355                 360
246
247   GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG      1275
248   Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
249       365                 370                 375
250
251   AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA      1323
252   Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
253   380                 385                 390                 395
254
255   CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA      1371
256   Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
257                 400                 405                 410
258
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